

Ashkenazi et al - SEQ ID NO: 3

RESULT 9

US-09-991-181-84

; Sequence 84, Application US/09991181

; Patent No. 6913919

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C53

; CURRENT APPLICATION NUMBER: US/09/991,181

; CURRENT FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match 66.8%; Score 3160; DB 2; Length 867;
Best Local Similarity 64.8%; Pred. No. 2.2e-303;
Matches 577; Conservative 120; Mismatches 140; Indels 54; Gaps 13;

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Db	5	SLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNI	64
Qy	64	NKTRKIMEHGGATFINAFVTTMCCPSRSSMLTGKYVHNHNVTNN	123
Db	65	NKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNVTNN	124
Qy	124	RTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWREWLGLIKNS	183
Db	125	RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNS	184
Qy	184	FDYAKDYFTDLITNESINYFKMSKRMYPHRPVMVISHAAPHGP	243
Db	185	SDYSKDYLTDLITNDSVSFRTSKKMYPHRPVLMVISHAAPHGP	244
Qy	244	HITPSYNYAPNMDKHWIMQYTGPMPLPIHMEFTNILQKRKLQT	303
Db	245	HITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRKLQT	304
Qy	304	GELentyIIYTADHGYHIGQFGLVKGKSMYPYDFDIRVPFFIR	363
Db	305	GELDNTYIVYTADHGYHIGQFGLVKGKSMYPYEFDIRVPFYVR	364
Qy	364	LAPTILDIAGLDTPPDVDGKSVLKLDDPEKPGNRFRTNKKAKI	423
Db	365	LAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKMRVWR	424
Qy	424	ESSKNIQQSNHLPKYERVKELCQQARYQTACEQPGQKWQCIED	483
Db	425	NDKVDAQEENFLPKYQRVKDLQRAEYQTACEQLGQKWQCVED	484
Qy	484	TVRQSTRNLYARGFHDKDKECSCRESGYRASRSQRKSQRQFLR	543
Db	485	GSR-ALSNLVPKYYGQGSEACTCDSGDYKLSLAGRR-KKL FKK	537
Qy	544	RSLSVEFEGEIIYDINLEEEEEELQVLQPRNIAKRHDEGHKGPR	603

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Db      584  GTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLHIDHEIETLQNKIK 643
Qy      659  NLREVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLKSHLHPFKEAAQEVD SKLQLFKE 718
Db      644  NLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHR--GSSLHPFRKGLQEKD-KVWLLRE 700
Qy      719  NNRRRKKEKRRQRKGEESLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNNNTYWC 778
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Qy      779  LRTVNETHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGY 838
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Db      820  KQCNPRTRNMDL---DGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG 867
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Emerson et al - Seq ID No: 3

RESULT 5

US-09-668-673B-16

; Sequence 16, Application US/09668673B

; Patent No. 6562956

; GENERAL INFORMATION:

; APPLICANT: Emerson, Charles P

; APPLICANT: Dhoot, Gurtej K

; TITLE OF INVENTION: IDENTIFICATION AND CLONING OF A NEW SUBFAMILY OF

; TITLE OF INVENTION: SULFATASES AND FUNCTIONAL EMBRYONIC TECHNIQUES FOR

; TITLE OF INVENTION: CHARACTERIZATION OF SUCH PROTEINS

; FILE REFERENCE: PENN-0733

; CURRENT APPLICATION NUMBER: US/09/668,673B

; CURRENT FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: 60/155,738

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 1611

; TYPE: PRT

; ORGANISM: Homo sapiens

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 818; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 SPSWQAMHEPRTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWREWLGLIKNSRFYNYTV 120

Qy     174 CRNGIKEKHGFDYAKDYFTDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQ 233
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Qy     414 ERGKFLRKKEESSKNIQQSNHLPKYERVKELCQQARYQTACEQPGQKWQCIEDTSGKLRI 473
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Qy     594 NRGRLADSSNAVGPPPTTVRVTHKCFILPNDSIH CERELYQSARAWKDHKAYIDKEIEAL 653
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Qy	654	QDKIKNLREVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLKSHLHPFKEAAQEVDSKL	713
Db	601	QDKIKNLREVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLKSHLHPFKEAAQEVDSKL	660
Qy	714	QLFKENRRRRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNN	773
Db	661	QLFKENRRRRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNN	720
Qy	774	NTYWCLRTVNETHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELR	833
Db	721	NTYWCLRTVNETHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELR	780
Qy	834	SCQGYKQCNPRPKNLDVGNKDGGSYDLHRGQLWDGWEG	871
Db	781	SCQGYKQCNPRPKNLDVGNKDGGSYDLHRGQLWDGWEG	818

Robertson et al.

RESULT 1

SULF1_HUMAN

ID SULF1_HUMAN STANDARD; PRT; 871 AA.
AC Q8IWU6; Q86YV8; Q8NCA2; Q9UPS5;
DT 19-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Extracellular sulfatase Sulf-1 precursor (EC 3.1.6.-) (HSulf-1).
GN Name=SULF1; Synonyms=KIAA1077;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], CHARACTERIZATION, AND MUTAGENESIS OF
RP 87-CYS-CYS-88.
RC TISSUE=Prostate;
RX MEDLINE=22370956; PubMed=12368295; DOI=10.1074/jbc.M205131200;
RA Morimoto-Tomita M., Uchimura K., Werb Z., Hemmerich S., Rosen S.D.;
RT "Cloning and characterization of two extracellular heparin-degrading
RT endosulfatases in mice and humans.";
RL J. Biol. Chem. 277:49175-49185(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], AND MUTAGENESIS OF 87-CYS-CYS-88.
RX MEDLINE=22692523; PubMed=12686563; DOI=10.1074/jbc.M302203200;
RA Lai J., Chien J., Staub J., Avula R., Greene E.L., Matthews T.A.,
RA Smith D.I., Kaufmann S.H., Roberts L.R., Shridhar V.;
RT "Loss of HSulf-1 up-regulates heparin-binding growth factor signaling
RT in cancer.";
RL J. Biol. Chem. 278:23107-23117(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 54-871.
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851; DOI=10.1093/dnares/6.3.197;
RA Kikuno R., Nagase T., Ishikawa K., Hirose M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 312-871.
RC TISSUE=Teratocarcinoma;
RX PubMed=14702039; DOI=10.1038/ngl285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 CC -!- FUNCTION: Exhibits arylsulfatase activity and highly specific
 CC endoglucosamine-6-sulfatase activity. It can remove sulfate from
 CC the C-6 position of glucosamine within specific subregions of
 CC intact heparin. Diminishes HSPG (heparan sulfate proteoglycans)
 CC sulfation, inhibits signaling by heparin-dependent growth factors,
 CC diminishes proliferation, and facilitates apoptosis in response to
 CC exogenous stimulation.
 CC -!- BIOPHYSICOCHEMICAL PROPERTIES:
 CC pH dependence:
 CC Optimum pH is 7.0-8.0;
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum and Golgi stack. Also
 CC localized on the cell surface (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed at highest levels in testis,
 CC stomach, skeletal muscle, lung, kidney, pancreas, small intestine
 CC and colon. It is also detected in normal ovarian surface
 CC epithelial cells. Down-regulation seen in ovarian carcinoma cell
 CC lines, ovarian cancers, breast, pancreatic, renal and
 CC hepatocellular carcinoma cell lines.
 CC -!- SIMILARITY: Belongs to the sulfatase family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY101175; AAM76860.1; -; mRNA.
 DR EMBL; AF545571; AA033315.1; -; mRNA.
 DR EMBL; AB029000; BAA83029.1; -; mRNA.
 DR EMBL; AK074873; BAC11258.1; -; mRNA.
 DR Ensembl; ENSG00000137573; Homo sapiens.
 DR HGNC; HGNC:20391; SULF1.
 DR GO; GO:0009986; C:cell surface; IDA.
 DR GO; GO:0005615; C:extracellular space; NAS.
 DR GO; GO:0004065; F:aryl sulfatase activity; IDA.
 DR GO; GO:0030201; P:heparan sulfate proteoglycan metabolism; NAS.
 DR InterPro; IPR000917; Sulfatase.
 DR Pfam; PF00884; Sulfatase; 1.
 DR PROSITE; PS00523; SULFATASE_1; 1.
 DR PROSITE; PS00149; SULFATASE_2; FALSE_NEG.
 KW Apoptosis; Endoplasmic reticulum; Glycoprotein; Golgi stack;
 KW Hydrolase; Signal.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 871 Extracellular sulfatase Sulf-1..
 FT /FTId=PRO_0000033434.
 FT MOD_RES 87 87 3-oxoalanine (Cys) (By similarity).
 FT CARBOHYD 64 64 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 111 111 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 131 131 N-linked (GlcNAc. . .) (Potential).

FT	CARBOHYD	148	148	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	170	170	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	197	197	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	240	240	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	623	623	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	773	773	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	783	783	N-linked (GlcNAc. . .) (Potential).
FT	MUTAGEN	87	88	CC->AA: Loss of arylsulfatase activity
FT				and loss of ability to modulate
FT				apoptosis.
FT	CONFLICT	49	49	L. -> P (in Ref. 2).
FT	CONFLICT	728	728	K -> R (in Ref. 4).
SQ	SEQUENCE	871 AA;	101027 MW;	9A90ADB280304364 CRC64;

Query Match 100.0%; Score 4729; DB 1; Length 871;
 Best Local Similarity 100.0%; Pred. No. 4.3e-274;
 Matches 871; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKYSCCALVLAVLGTLLGSLCSTVRSRFRGRIQQERKNIRPNILVLTDDQDVELGSL	60
Db	1	MKYSCCALVLAVLGTLLGSLCSTVRSRFRGRIQQERKNIRPNILVLTDDQDVELGSL	60
Qy	61	QVMNKTRKIMEHGGATFINAFVTTMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAM	120
Db	61	QVMNKTRKIMEHGGATFINAFVTTMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAM	120
Qy	121	HEPRTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWREWLGLIKNSRFYNYTVCRNGIKE	180
Db	121	HEPRTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWREWLGLIKNSRFYNYTVCRNGIKE	180
Qy	181	KHGFYDIAKDYFTDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPN	240
Db	181	KHGFYDIAKDYFTDLITNESINYFKMSKRMYPHRPVMVISHAAPHGPEDSAPQFSKLYPN	240
Qy	241	ASQHITPSYNYAPNMDKHWIMQYTGPMPLPIHMEFTNILQRKRLQTLMSVDDSVRLYNML	300
Db	241	ASQHITPSYNYAPNMDKHWIMQYTGPMPLPIHMEFTNILQRKRLQTLMSVDDSVRLYNML	300
Qy	301	VETGELENTYIIYTADHGYHIGQFGLVKGKSMFYDFDIRVPFFIRGPSVEPGSIVPQIVL	360
Db	301	VETGELENTYIIYTADHGYHIGQFGLVKGKSMFYDFDIRVPFFIRGPSVEPGSIVPQIVL	360
Qy	361	NIDLAPTILDIAGLDTTPDVGKSVLKLDPKPGNRFRFTNKKAKIWRDTFLVERGKFLR	420
Db	361	NIDLAPTILDIAGLDTTPDVGKSVLKLDPKPGNRFRFTNKKAKIWRDTFLVERGKFLR	420
Qy	421	KKEESSKNIQQSNHLPKYERVKELCQARYQTACEQPGQKWQCIEDTSGKLRHCKGKPS	480
Db	421	KKEESSKNIQQSNHLPKYERVKELCQARYQTACEQPGQKWQCIEDTSGKLRHCKGKPS	480
Qy	481	DLTTRVQSTRNLYARGFHDKDKECSCRESGYRASRSQRKSQRQFLRNQGTPKYKPRFVHT	540
Db	481	DLTTRVQSTRNLYARGFHDKDKECSCRESGYRASRSQRKSQRQFLRNQGTPKYKPRFVHT	540
Qy	541	RQTRSLSVFEGEIIYDINLEEEELQVLQPRNIAKRHDEGHKGPRDLQASSGGNRGRMLA	600
Db	541	RQTRSLSVFEGEIIYDINLEEEELQVLQPRNIAKRHDEGHKGPRDLQASSGGNRGRMLA	600
Qy	601	DSSNAVGPPTTVRVTHKCFILPNDSIHCCERELYQSARAWKDHKAYIDKEIEALQDKIKNL	660
Db	601	DSSNAVGPPTTVRVTHKCFILPNDSIHCCERELYQSARAWKDHKAYIDKEIEALQDKIKNL	660

Qy	661	REVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLSHLHPFKEAAQEVD SKLQLFKENN	720
Db	661	REVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLSHLHPFKEAAQEVD SKLQLFKENN	720
Qy	721	RRRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNNNTYWCLR	780
Db	721	RRRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTSSNNNTYWCLR	780
Qy	781	TVNETHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQ	840
Db	781	TVNETHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQ	840
Qy	841	CNPRPKNLDVGNKDGGSYDLHRGQLWDGWEG	871
Db	841	CNPRPKNLDVGNKDGGSYDLHRGQLWDGWEG	871

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4729	100.0	871	4	US-10-177-293-248	Sequence 248, App
2	4729	100.0	871	4	US-10-265-071-3	Sequence 3, Appli
3	4729	100.0	871	4	US-10-025-966A-3	Sequence 3, Appli
4	4729	100.0	871	4	US-10-314-881-3	Sequence 3, Appli
5	4729	100.0	871	4	US-10-426-776-11	Sequence 11, Appl
6	4729	100.0	871	4	US-10-734-564-76	Sequence 76, Appl
7	4729	100.0	871	5	US-10-775-678-29	Sequence 29, Appl
8	4729	100.0	871	5	US-10-825-198-3	Sequence 3, Appli
9	4729	100.0	871	5	US-10-994-117-9	Sequence 9, Appli
10	4729	100.0	871	5	US-10-450-186-20	Sequence 20, Appl
11	4729	100.0	871	5	US-10-991-287-9	Sequence 9, Appli
12	4729	100.0	871	5	US-10-933-025-3	Sequence 3, Appli
13	4729	100.0	871	5	US-10-518-184-1	Sequence 1, Appli
14	4729	100.0	871	6	US-11-051-720-1419	Sequence 1419, Ap
15	4729	100.0	871	6	US-11-051-720-1586	Sequence 1586, Ap
16	4729	100.0	871	6	US-11-219-360-3	Sequence 3, Appli
17	4725	99.9	871	6	US-11-051-720-1697	Sequence 1697, Ap
18	4722	99.9	871	5	US-10-991-321-26	Sequence 26, Appl
19	4460	94.3	818	3	US-09-833-790-366	Sequence 366, App
20	4460	94.3	818	5	US-10-723-860-543	Sequence 543, App
21	4460	94.3	1611	4	US-10-389-532-16	Sequence 16, Appl
22	4364	92.3	800	4	US-10-296-115-1229	Sequence 1229, Ap
23	4237	89.6	791	6	US-11-051-720-1290	Sequence 1290, Ap
24	4105	86.8	867	4	US-10-389-532-2	Sequence 2, Appli
25	4102	86.7	790	6	US-11-051-720-1289	Sequence 1289, Ap
26	3999	84.6	751	6	US-11-051-720-1760	Sequence 1760, Ap
27	3395	71.8	630	6	US-11-051-720-1580	Sequence 1580, Ap
28	3179.5	67.2	870	3	US-09-833-245-650	Sequence 650, App
29	3179.5	67.2	870	4	US-10-182-951-5	Sequence 5, Appli
30	3179.5	67.2	870	4	US-10-265-071-6	Sequence 6, Appli
31	3179.5	67.2	870	4	US-10-265-071-15	Sequence 15, Appl
32	3179.5	67.2	870	4	US-10-025-966A-6	Sequence 6, Appli
33	3179.5	67.2	870	4	US-10-025-966A-15	Sequence 15, Appl
34	3179.5	67.2	870	5	US-10-775-678-31	Sequence 31, Appl
35	3179.5	67.2	870	5	US-10-933-025-6	Sequence 6, Appli
36	3179.5	67.2	870	5	US-10-933-025-15	Sequence 15, Appl
37	3179.5	67.2	870	6	US-11-219-360-6	Sequence 6, Appli
38	3179.5	67.2	870	6	US-11-219-360-15	Sequence 15, Appl
39	3179.5	67.2	870	6	US-11-264-096-650	Sequence 650, App
40	3178.5	67.2	870	3	US-09-833-245-649	Sequence 649, App
41	3178.5	67.2	870	4	US-10-264-237-2754	Sequence 2754, Ap
42	3178.5	67.2	870	6	US-11-264-096-649	Sequence 649, App
43	3175.5	67.1	870	3	US-09-970-287-2	Sequence 2, Appli
44	3175.5	67.1	870	6	US-11-066-098-2	Sequence 2, Appli

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4729	100.0	871	7	US-11-313-836-11	Sequence 11, Appl
2	4729	100.0	871	7	US-11-105-233-140	Sequence 140, App
3	4729	100.0	871	7	US-11-043-842-96	Sequence 96, Appl
4	4725	99.9	871	7	US-11-043-842-840	Sequence 840, App
5	4722	99.9	871	6	US-10-700-439-103	Sequence 103, App
6	4722	99.9	871	7	US-11-316-132-1	Sequence 1, Appli
7	4406.5	93.2	870	7	US-11-316-132-2	Sequence 2, Appli
8	4237	89.6	791	7	US-11-043-842-98	Sequence 98, Appl
9	4105	86.8	867	7	US-11-316-132-3	Sequence 3, Appli
10	4102	86.7	790	7	US-11-043-842-97	Sequence 97, Appl
11	3999	84.6	751	7	US-11-043-842-1006	Sequence 1006, Ap
12	3179.5	67.2	870	7	US-11-316-132-4	Sequence 4, Appli
13	2244	47.5	416	7	US-11-043-842-99	Sequence 99, Appl
14	2142	45.3	410	7	US-11-043-842-100	Sequence 100, App
15	1025	21.7	210	7	US-11-043-842-101	Sequence 101, App
16	730	15.4	145	7	US-11-043-842-102	Sequence 102, App
17	280	5.9	536	6	US-10-527-101-12	Sequence 12, Appl
18	238	5.0	40	7	US-11-043-842-841	Sequence 841, App
19	208	4.4	515	6	US-10-196-749-76	Sequence 76, Appl
20	207.5	4.4	599	7	US-11-313-836-13	Sequence

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4729	100.0	871	1	SULF1_HUMAN	Q8iwu6 homo sapien
2	4725	99.9	871	2	Q7Z2W2_HUMAN	Q7z2w2 homo sapien
3	4450	94.1	869	2	Q32KH2_CANFA	Q32kh2 canis famil
4	4406.5	93.2	870	1	SULF1_RAT	Q8vi60 rattus norv
5	4393.5	92.9	870	1	SULF1_MOUSE	Q8k007 mus musculu
6	4159.5	88.0	1079	2	Q6ZPZ0_MOUSE	Q6zpz0 mus musculu
7	4105	86.8	867	1	SULF1_COTCO	Q90xb6 coturnix co
8	3478	73.5	874	2	Q6EFA0_BRARE	Q6efa0 brachydanio
9	3473.5	73.5	892	2	Q6EF99_BRARE	Q6ef99 brachydanio
10	3413.5	72.2	1099	2	Q6EFA1_BRARE	Q6efa1 brachydanio
11	3330	70.4	644	2	Q6NUJ9_HUMAN	Q6nuj9 homo sapien
12	3210	67.9	877	2	Q5UAX9_COTCO	Q5uax9 coturnix co
13	3195	67.6	1160	2	Q4SFB1_TETNG	Q4sfb1 tetraodon n
14	3179.5	67.2	870	1	SULF2_HUMAN	Q8iwu5 homo sapien
15	3179.5	67.2	870	2	Q5JYE1_HUMAN	Q5jye1 homo sapien
16	3165	66.9	869	2	Q32KH1_CANFA	Q32kh1 canis famil
17	3149	66.6	875	1	SULF2_MOUSE	Q8cfg0 mus musculu
18	3149	66.6	948	2	Q6ZPV3_MOUSE	Q6zpv3 mus musculu
19	3146	66.5	875	2	Q3TNM3_MOUSE	Q3tnm3 m 12 days e
20	3144	66.5	875	2	Q3L472_RAT	Q3l472 rattus norv
21	3136	66.3	875	2	Q6GL29_XENTR	Q6gl29 xenopus tro
22	3107	65.7	866	2	Q32KJ3_RAT	Q32kj3 rattus norv
23	3086	65.3	867	2	Q6EF97_BRARE	Q6ef97 brachydanio
24	3067	64.9	885	2	Q6EF98_BRARE	Q6ef98 brachydanio
25	2777	58.7	873	2	Q7ZVU8_BRARE	Q7zvu8 brachydanio
26	2721.5	57.5	879	2	Q4SZ41_TETNG	Q4sz41 tetraodon n
27	2701	57.1	1239	2	Q4SR77_TETNG	Q4sr77 tetraodon

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1607	34.0	709	2	T16584	hypothetical prote
2	829.5	17.5	552	1	KJHUGU	N-acetylglucosamin
3	468.5	9.9	649	2	S43229	arylsulfatase (EC
4	440	9.3	639	2	T46577	arylsulfatase (EC
5	355	7.5	646	1	KJKM	arylsulfatase (EC
6	309	6.5	497	2	G65169	probable sulfatase
7	307	6.5	497	2	C91206	probable sulfatase
8	307	6.5	497	2	E86052	probable sulfatase
9	276.5	5.8	571	2	E64903	arylsulfatase homo
10	276.5	5.8	571	2	G90891	probable sulfatase
11	275.5	5.8	535	2	AF0103	probable sulfatase
12	275.5	5.8	571	2	B85726	probable sulfatase
13	266	5.6	557	2	AF0370	probable sulfatase
14	254.5	5.4	550	1	KJHUID	iduronate-2-sulfat
15	240	5.1	563	2	A47153	iduronate-2-sulfat
16	239.5	5.1	517	2	AB0102	probable sulfatase
17	238.5	5.0	583	1	KJHUAC	steryl-

Database : Issued_Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4729	100.0	871	2	US-09-773-426A-3	Sequence 3, Appli
2	4729	100.0	871	2	US-10-314-881-3	Sequence 3, Appli
3	4729	100.0	871	2	US-09-495-823-3	Sequence 3, Appli
4	4729	100.0	871	3	US-10-426-776-11	Sequence 11, Appl
5	4460	94.3	1611	2	US-09-668-673B-16	Sequence 16, Appl
6	4460	94.3	1611	2	US-10-389-532-16	Sequence 16, Appl
7	4105	86.8	867	2	US-09-668-673B-2	Sequence 2, Appli
8	4105	86.8	867	2	US-10-389-532-2	Sequence 2, Appli
9	3160	66.8	867	2	US-09-991-181-84	Sequence 84, Appl
10	3160	66.8	867	2	US-09-990-444-84	Sequence 84, Appl
11	3160	66.8	867	2	US-09-997-333-84	Sequence 84, Appl
12	3160	66.8	867	2	US-09-992-598-84	Sequence 84, Appl
13	3160	66.8	867	2	US-09-989-735-84	Sequence 84, Appl
14	3160	66.8	867	3	US-09-989-726-84	Sequence 84, Appl
15	3160	66.8	867	3	US-09-997-514-84	Sequence 84, Appl
16	3160	66.8	867	3	US-09-989-728-84	Sequence 84, Appl
17	3160	66.8	867	3	US-09-997-349-84	Sequence 84, Appl
18	3160	66.8	867	3	US-09-997-653-84	Sequence 84, Appl
19	3160	66.8	867	3	US-09-989-293A-84	Sequence 84, Appl
20	2418	51.1	690	2	US-09-886-319A-36	Sequence 36, Appl
21	1950	41.2	360	2	US-09-810-347-4	Sequence 4, Appli
22	1927.5	40.8	372	2	US-09-810-347-2	Sequence 2, Appli
23	1681	35.5	307	2	US-09-810-347-5	Sequence 5, Appli
24	1607	34.0	709	2	US-09-668-673B-3	Sequence 3, Appli
25	1607	34.0	709	2	US-10-389-532-3	Sequence 3, Appli
26	1245	26.3	455	2	US-09-668-673B-14	Sequence 14, Appl
27	1245	26.3	455	2	US-10-389-532-14	Sequence 14, Appl
28	1172	24.8	309	2	US-09-810-347-6	Sequence 6, Appli
29	1021	21.6	196	2	US-09-668-673B-18	Sequence 18, Appl
30	1021	21.6	196	2	US-10-389-532-18	Sequence 18, Appl
31	956.5	20.2	470	2	US-09-886-319A-35	Sequence 35, Appl
32	807	17.1	160	2	US-09-668-673B-7	Sequence 7, Appli
33	807	17.1	160	2	US-10-389-532-7	Sequence 7, Appli
34	801.5	16.9	510	1	US-08-484-493-11	Sequence 11, Appl
35	801.5	16.9	510	1	US-08-484-494-11	Sequence 11, Appl
36	801.5	16.9	510	1	US-08-345-212-11	Sequence 11, Appl
37	801.5	16.9	510	2	US-09-249-003-11	Sequence 11, Appl
38	801.5	16.9	510	2	US-09-685-844-11	Sequence 11, Appli
39	506	10.7	96	2	US-09-668-673B-20	Sequence 20, Appl
40	506	10.7	96	2	US-10-389-532-20	Sequence 20, Appl
41	406.5	8.6	387	2	US-09-270-767-33219	Sequence 33219, A
42	406.5	8.6	387	2	US-09-270-767-48436	Sequence 48436, A
43	381.5	8.1	520	2	US-09-773-426A-10	Sequence 10, Appl

44	381.5	8.1	520	2	US-10-314-881-10	Sequence 10, Appl
45	334.5	7.1	552	2	US-09-773-426A-9	Sequence 9, Appli

Database : A_Geneseq_8:*

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- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4729	100.0	871	3	AAB00191	Aab00191 Breast ca
2	4729	100.0	871	4	AAB85481	Aab85481 Human 235
3	4729	100.0	871	5	ABG69640	Abg69640 Human sec
4	4729	100.0	871	5	ABG71835	Abg71835 Human SUL
5	4729	100.0	871	6	ABR47506	Abr47506 Breast ca
6	4729	100.0	871	6	ABU63345	Abu63345 Human sul
7	4729	100.0	871	7	ADH60968	Adh60968 Human 235
8	4729	100.0	871	8	ADH58926	Adh58926 Glucosami
9	4729	100.0	871	8	ADJ57910	Adj57910 Human 235
10	4729	100.0	871	8	ADN16189	Adn16189 Human sul
11	4729	100.0	871	8	ADQ29650	Adq29650 Human col
12	4729	100.0	871	8	ADR21250	Adr21250 Human ext
13	4729	100.0	871	8	ADU47472	Adu47472 Human 235
14	4729	100.0	871	9	AEA54851	Aea54851 Human tum
15	4729	100.0	871	9	AEC03934	Aec03934 Human bre
16	4729	100.0	871	10	AEF69962	Aef69962 Colorecta
17	4725	99.9	871	9	AEC04654	Aec04654 Human bre
18	4722	99.9	871	9	ADY25735	Ady25735 SULF rela
19	4722	99.9	871	9	ADZ09831	Adz09831 Human bre
20	4722	99.9	871	9	AEA04458	Aea04458 Human pro
21	4722	99.9	871	9	ADZ87322	Adz87322 Human sul
22	4722	99.9	871	9	AEE39581	Aee39581 Human sul
23	4712	99.6	871	9	AEE39599	Aee39599 Human sul
24	4608	97.4	871	8	ADN16208	Adn16208 Mouse sul
25	4474.5	94.6	828	8	ABM85153	Abm85153 Human dia
26	4460	94.3	818	5	AAU69417	Aau69417 Lung smal
27	4460	94.3	818	8	ADQ17726	Adq17726 Human sof
28	4460	94.3	1611	4	AAE00438	Aae00438 Human sul
29	4398.5	93.0	820	8	ABM85154	Abm85154 Human dia
30	4364	92.3	800	4	AAM25714	Aam25714 Human pro
31	4364	92.3	800	7	ADE09946	Ade09946 Novel pro
32	4237	89.6	791	9	AEC03936	Aec03936 Human bre
33	4105	86.8	867	4	AAE00434	Aae00434 Quail sul
34	4101	86.7	761	9	AEC04854	Aec04854 Human bre
35	4039	85.4	790	9	AEC03935	Aec03935 Human bre
36	3999	84.6	734	9	AEC04859	Aec04859 Human bre
37	3999	84.6	751	9	AEC04858	Aec04858 Human bre
38	3995	84.5	733	9	AEC04857	Aec04857 Human bre
39	3198.5	67.6	852	9	AEE39583	Aee39583 Human sul
40	3188.5	67.4	852	9	AEE39600	Aee39600 Human sul

41	3179.5	67.2	870	4	AAE01440	Aae01440 Human gen
42	3179.5	67.2	870	4	AAB85774	Aab85774 Human dru
43	3179.5	67.2	870	4	AAM79215	Aam79215 Human pro
44	3179.5	67.2	870	5	ABG63903	Abg63903 Human alb
45	3179.5	67.2	870	5	ABG71836	Abg71836 human SUL